SEQUENCE LISTING

<110> LIN, LEU-FEN H
COLLINS, FRANKLIN D
DOHERTY, DANIEL H
LILE, JACK
BEKTESH, SUSAN

<120> Glial Cell Line-Derived Neurotrophic Factor

<130> S-225E Rev 070302

<140> 08/182,183
<141> 1994-05-23

<150> 07/764,685
<151> 1991-09-20

<150> 07/774,109
<151> 1991-10-08

<150> 07/788,423
<151> 1991-11-06

<150> 07/855,413
<151> 1992-03-19

<150> PCT/US92/07888
<151> 1992-09-17

<160> 29

<170> PatentIn version 3.1

<210> 1

<211> 25

<212> PRT

<213> Rattus rattus

<220>

<221> MISC_FEATURE

<222> (16)..(16)

<223> Xaa in position 16 may be any one of the 20 naturally occurring a
mino acids.

<220>

<221> MISC_FEATURE

<223> N-terminal fragment

<400> 1

Ser Pro Asp Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Xaa
1 5 10 15

Gln Ala Ala Ala Ala Ser Pro Asp Asn
20 25

<210> 2

<211> 13

<212> PRT

<213> Rattus rattus

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> Xaa in position 2 is either Lys or Gln

<220>

<221> MISC_FEATURE

<223> Internal GDNF peptide fragment

<400> 2

Asp Xaa Ile Leu Lys Asn Leu Gly Arg Val Arg Arg Leu
1 5 10

<210> 3

<211> 900

<212> DNA

<213> Rattus rattus

<220>

<221> CDS

<222> (25)..(705)

<223>

<220>

<221> mat_peptide

<222> (304)..()

<223>

<400> 3

```
ccccgggct gcaggaattc gggg gtc tac gga gac cgg atc cga ggt gcc        51
                          Val Tyr Gly Asp Arg Ile Arg Gly Ala
                                      -90                 -85

gcc gcc gga cgg gac tct aag atg aag tta tgg gat gtc gtg gct gtc        99
Ala Ala Gly Arg Asp Ser Lys Met Lys Leu Trp Asp Val Val Ala Val
               -80                 -75                 -70

tgc ctg gtg ttg ctg cac acc gcg tct gcc ttc ccg ctg ccc gcc ggt       147
Cys Leu Val Leu Leu His Thr Ala Ser Ala Phe Pro Leu Pro Ala Gly
            -65                 -60                 -55

aag agg ctt ctc gaa gcg ccc gcc gaa gac cac tcc ctc ggc cac cgc       195
Lys Arg Leu Leu Glu Ala Pro Ala Glu Asp His Ser Leu Gly His Arg
        -50                 -45                 -40

cgc gtg ccc ttc gcg ctg acc agt gac tcc aat atg ccc gaa gat tat       243
Arg Val Pro Phe Ala Leu Thr Ser Asp Ser Asn Met Pro Glu Asp Tyr
    -35                 -30                 -25
```

```
cct gac cag ttt gat gac gtc atg gat ttt att caa gcc acc atc aaa      291
Pro Asp Gln Phe Asp Asp Val Met Asp Phe Ile Gln Ala Thr Ile Lys
-20                 -15                 -10                 -5

aga ctg aaa agg tca cca gat aaa caa gcg gcg gca ctt cct cga aga      339
Arg Leu Lys Arg Ser Pro Asp Lys Gln Ala Ala Ala Leu Pro Arg Arg
           -1  1                5                  10

gag agg aac cgg caa gct gca gct gcc agc cca gag aat tcc aga ggg      387
Glu Arg Asn Arg Gln Ala Ala Ala Ala Ser Pro Glu Asn Ser Arg Gly
        15                  20                  25

aaa ggt cgc aga ggc cag agg ggc aaa aat cgg ggg tgc gtc tta act      435
Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr
    30                  35                  40

gca ata cac tta aat gtc act gac ttg ggt ttg ggc tac gaa acc aag      483
Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys
45                  50                  55                  60

gag gaa ctg atc ttt cga tat tgt agc ggt tcc tgt gaa gcg gcc gag      531
Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys Glu Ala Ala Glu
                65                  70                  75

aca atg tac gac aaa ata cta aaa aat ctg tct cga agt aga agg cta      579
Thr Met Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg Ser Arg Arg Leu
           80                  85                  90

aca agt gac aag gta ggc cag gca tgt tgc agg ccg gtc gcc ttc gac      627
Thr Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro Val Ala Phe Asp
        95                  100                 105

gac gac ctg tcg ttt tta gac gac agc ctg gtt tac cat atc cta aga      675
Asp Asp Leu Ser Phe Leu Asp Asp Ser Leu Val Tyr His Ile Leu Arg
    110                 115                 120

aag cat tcc gct aaa cgg tgt gga tgt atc tgaccctggc tccagagact       725
Lys His Ser Ala Lys Arg Cys Gly Cys Ile
125                 130

gctgtgtatt gcattcctgc tacactgcga agaaagggac caaggttccc aggaaatatt    785

tgcccagaaa ggaagataag gaccaagaag gcagaggcag aggcggaaga agaagaagaa    845

aagaaggacg aaggcagcca tctgtgggag cctgtagaag gaggcccagc tacag         900
```

<210> 4

<211> 227

<212> PRT

<213> Rattus rattus

<400> 4

```
Val Tyr Gly Asp Arg Ile Arg Gly Ala Ala Ala Gly Arg Asp Ser Lys
           -90                 -85                 -80
```

```
Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
        -75                 -70                 -65

Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Leu Leu Glu Ala Pro
    -60                 -55                 -50

Ala Glu Asp His Ser Leu Gly His Arg Arg Val Pro Phe Ala Leu Thr
-45                 -40                 -35                 -30

Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val
                -25                 -20                 -15

Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp
            -10                 -5              -1  1

Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala
    5                   10                  15

Ala Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg
20                  25                  30                  35

Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr
                40                  45                  50

Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr
            55                  60                  65

Cys Ser Gly Ser Cys Glu Ala Ala Glu Thr Met Tyr Asp Lys Ile Leu
        70                  75                  80

Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp Lys Val Gly Gln
    85                  90                  95

Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
100                 105                 110                 115

Asp Ser Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys
                120                 125                 130

Gly Cys Ile
```

<210> 5

<211> 562

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (24)..(506)

<223>

<220>

<221> mat_peptide

<222> (105)..()

<223>

<400> 5

```
attttctctt ttctttttga aca agc aat atg cca gag gat tat cct gat cag     53
                           Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln
                                  -25                 -20

ttc gat gat gtc atg gat ttt att caa gcc acc att aaa aga ctg aaa     101
Phe Asp Asp Val Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys
        -15                 -10                 -5

agg tca cca gat aaa caa atg gca gtg ctt cct aga aga gag cgg aat     149
Arg Ser Pro Asp Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn
-1  1               5                  10                  15

cgg cag gct gca gct gcc aac cca gag aat tcc aga gga aaa ggt cgg     197
Arg Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg
                20                  25                  30

aga ggc cag agg ggc aaa aac cgg ggt tgt gtc tta act gca ata cat     245
Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His
            35                  40                  45

tta aat gtc act gac ttg ggt ctg ggc tat gaa acc aag gag gaa ctg     293
Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu
        50                  55                  60

att ttt agg tac tgc agc ggc tct tgc gat gca gct gag aca acg tac     341
Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr
    65                  70                  75

gac aaa ata ttg aaa aac tta tcc aga aat aga agg ctg gtg act gac     389
Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Thr Asp
80                  85                  90                  95

aaa gta ggg cag gca tgt tgc aga ccc atc gcc ttt gat gat gac ctg     437
Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu
                100                 105                 110

tcg ttt tta gat gat aac ctg gtt tac cat att cta aga aag cat tcc     485
Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser
            115                 120                 125
```

gct aaa agg tgt gga tgt atc tgactccggc tccagagact gctgtgtatt 536
Ala Lys Arg Cys Gly Cys Ile
130

gcattcctgc tacagtgcaa agaaag 562

<210> 6

<211> 161

<212> PRT

<213> Homo sapiens

<400> 6

Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val Met Asp
-25 -20 -15

Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp Lys Gln
-10 -5 -1 1 5

Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala Ala
10 15 20

Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys
25 30 35

Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu
40 45 50

Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser
55 60 65

Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn
70 75 80 85

Leu Ser Arg Asn Arg Arg Leu Val Thr Asp Lys Val Gly Gln Ala Cys
90 95 100

Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn
105 110 115

Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys
120 125 130

Ile

<210> 7

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide probe

<220>

<221> misc_feature

<222> (3)..(3)

<223> N at position 3 is inosine

<220>

<221> misc_feature

<222> (15)..(15)

<223> N at position 15 is inosine

<220>

<221> misc_feature

<222> (18)..(18)

<223> N at position 18 is inosine

<400> 7
ccngayaarc argcngcngc 20

<210> 8

<211> 223

<212> DNA

<213> Homo sapiens

<400> 8
ttctctcccc cacctcccgc ctgcccgcgc aggtgccgcc gccggacggg actttaagat 60

gaagttatgg gatgtcgtgg ctgtctgcct ggtgctgctc cacaccgcgt ccgccttccc 120

gctgcccgcc ggtaagaggc ctcccgaggc gcccgccgaa gaccgctccc tcggccgccg 180

ccgcgcgccc ttcgcgctga gcagtgactg taagaaccgt tcc 223

<210> 9

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 9
cccgaattcg gg 12

<210> 10

<211> 7

<212> PRT

<213> Rattus rattus

<400> 10

Pro Asp Lys Gln Ala Ala Ala
1 5

<210> 11

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleic acid sequence from pBluescript SK-76.1 encoding rat GDNF N-terminus sequence

<400> 11
gagaggaacc ggcaagctgc wgmwgymwgm ccw 33

<210> 12

<211> 11

<212> PRT

<213> Rattus rattus

<400> 12

Glu Arg Asn Arg Gln Ala Ala Ala Ala Ser Pro
1 5 10

<210> 13

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Oligonucleotide PCR primer DHD-26 to amplify DNA encoding rat GDNF polypeptide

<220>

<221> misc_feature

<222> (9)..(9)

<223> N at position 9 is inosine

<220>

<221> misc_feature

<222> (12)..(12)

<223> N at position 12 is inosine

<400> 13
arrttyttna rnatyttrtc 20

<210> 14

<211> 7

<212> PRT

<213> Rattus rattus

<220>

<221> misc_feature

<223> Internal rat GDNF peptide

<400> 14

Asp Lys Ile Leu Lys Asn Leu
1 5

<210> 15

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer PD1 to amplify rat GDNF probe

<400> 15
gacgggactc taagatg 17

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer DHD23 to amplify rat GDNF probe

<220>

<221> misc_feature

<222> (3)..(3)

<223> N at position 3 is inosine

<220>

<221> misc_feature

<222> (6)..(6)

<223> N at position 3 is inosine

<220>

<221> misc_feature

<222> (18)..(18)

<223> N at position 3 is inosine

<400> 16
gcngcngcyt gyttrtcngg 20

<210> 17

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer LF2 to amplify rat GDNF probe

<400> 17
cgagacaatg tacgaca 17

<210> 18

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer PD2 to amplify rat GDNF probe

<400> 18
ctctggagcc agggtca 17

<210> 19

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer PD1 to amplify rat GDNF probe

<400> 19
cccgaattcg acgggactct aagatg 26

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer LFA to amplify rat GDNF probe

<400> 20
cggtggccag agggagtggt cttc 24

<210> 21

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer PD3 to amplify human cDNA

<400> 21
cgcggatcca ataaggagga aaaaaaatgt caccagataa acaaat 46

<210> 22

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer PD4 to amplify human cDNA

<400> 22
cgcggtaccc agtctctgga gccgga 26

<210> 23

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic adapter fragment for plasmid pCJ1

<400> 23
gatctagaat tgtcatgttt gacagcttat cat 33

<210> 24

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Polylinker sequence for plasmid pCJX1-1 with EcoRI and PSTI overh
angs

<400> 24
aattcccggg taccagatct gagctcacta gtctgca 37

<210> 25

<211> 747

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (32)..(691)

<223>

<220>

<221> mat_peptide

<222> (290)..()

<223>

<400> 25
ttctctcccc cacctcccgc ctgcccgcgc a ggt gcc gcc gcc gga cgg gac 52
Gly Ala Ala Ala Gly Arg Asp
-85 -80

```
ttt aag atg aag tta tgg gat gtc gtg gct gtc tgc ctg gtg ctg ctc      100
Phe Lys Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu
                -75                 -70                 -65

cac acc gcg tcc gcc ttc ccg ctg ccc gcc ggt aag agg cct ccc gag      148
His Thr Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu
            -60                 -55                 -50

gcg ccc gcc gaa gac cgc tcc ctc ggc cgc cgc cgc gcg ccc ttc gcg      196
Ala Pro Ala Glu Asp Arg Ser Leu Gly Arg Arg Arg Ala Pro Phe Ala
        -45                 -40                 -35

ctg agc agt gac tca aat atg cca gag gat tat cct gat cag ttc gat      244
Leu Ser Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp
    -30                 -25                 -20

gat gtc atg gat ttt att caa gcc acc att aaa aga ctg aaa agg tca      292
Asp Val Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser
-15                 -10                 -5                  -1  1

cca gat aaa caa atg gca gtg ctt cct aga aga gag cgg aat cgg cag      340
Pro Asp Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln
            5                   10                  15

gct gca gct gcc aac cca gag aat tcc aga gga aaa ggt cgg aga ggc      388
Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly
        20                  25                  30

cag agg ggc aaa aac cgg ggt tgt gtc tta act gca ata cat tta aat      436
Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn
    35                  40                  45

gtc act gac ttg ggt ctg ggc tat gaa acc aag gag gaa ctg att ttt      484
Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe
50                  55                  60                  65

agg tac tgc agc ggc tct tgc gat gca gct gag aca acg tac gac aaa      532
Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys
                70                  75                  80

ata ttg aaa aac tta tcc aga aat aga agg ctg gtg act gac aaa gta      580
Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Thr Asp Lys Val
            85                  90                  95

ggg cag gca tgt tgc aga ccc atc gcc ttt gat gat gac ctg tcg ttt      628
Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe
        100                 105                 110

tta gat gat aac ctg gtt tac cat att cta aga aag cat tcc gct aaa      676
Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys
    115                 120                 125

agg tgt gga tgt atc tgactccggc tccagagact gctgtgtatt gcattcctgc      731
Arg Cys Gly Cys Ile
130

tacagtgcaa agaaag                                                   747
```

<210> 26

<211> 220

<212> PRT

<213> Homo sapiens

<400> 26

```
Gly Ala Ala Ala Gly Arg Asp Phe Lys Met Lys Leu Trp Asp Val Val
    -85                 -80                 -75

Ala Val Cys Leu Val Leu Leu His Thr Ala Ser Ala Phe Pro Leu Pro
-70                 -65                 -60                 -55

Ala Gly Lys Arg Pro Pro Glu Ala Pro Ala Glu Asp Arg Ser Leu Gly
                -50                 -45                 -40

Arg Arg Arg Ala Pro Phe Ala Leu Ser Ser Asp Ser Asn Met Pro Glu
            -35                 -30                 -25

Asp Tyr Pro Asp Gln Phe Asp Asp Val Met Asp Phe Ile Gln Ala Thr
        -20                 -15                 -10

Ile Lys Arg Leu Lys Arg Ser Pro Asp Lys Gln Met Ala Val Leu Pro
    -5              -1  1                   5                   10

Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser
                15                  20                  25

Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val
            30                  35                  40

Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu
        45                  50                  55

Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala
    60                  65                  70

Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg
75                  80                  85                  90

Arg Leu Val Thr Asp Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala
                95                  100                 105

Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile
            110                 115                 120

Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys Ile
        125                 130
```

<210> 27

<211> 211

<212> PRT

<213> Rattus rattus

<220>

<221> MISC_FEATURE

<223> Rat pre-pro GDNF

<400> 27

```
Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
1               5                  10                  15

Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Leu Leu Glu Ala Pro
            20                  25                  30

Ala Glu Asp His Ser Leu Gly His Arg Arg Val Pro Phe Ala Leu Thr
        35                  40                  45

Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val
    50                  55                  60

Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp
65                  70                  75                  80

Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala
                85                  90                  95

Ala Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg
            100                 105                 110

Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr
        115                 120                 125

Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr
    130                 135                 140

Cys Ser Gly Ser Cys Glu Ala Ala Glu Thr Met Tyr Asp Lys Ile Leu
145                 150                 155                 160

Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp Lys Val Gly Gln
                165                 170                 175
```

Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
180 185 190

Asp Ser Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys
195 200 205

Gly Cys Ile
210

<210> 28

<211> 211

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> Human pre-pro GDNF

<400> 28

Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
1 5 10 15

Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu Ala Pro
20 25 30

Ala Glu Asp Arg Ser Leu Gly Arg Arg Arg Ala Pro Phe Ala Leu Ser
35 40 45

Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val
50 55 60

Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp
65 70 75 80

Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala
85 90 95

Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg
100 105 110

Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr
115 120 125

Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr
130 135 140

Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu
145 150 155 160

Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Thr Asp Lys Val Gly Gln
165 170 175

Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
180 185 190

Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys
195 200 205

Gly Cys Ile
210

<210> 29

<211> 50

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Human pre-pro GDNF N-terminal fragment

<400> 29

Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
1 5 10 15

Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu Ala Pro
20 25 30

Ala Glu Asp Arg Ser Leu Gly Arg Arg Arg Ala Pro Phe Ala Leu Ser
35 40 45

Ser Asp
50